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# Nitrogen Harvest Index Variation in *Avena Sativa* and *A. Sterilis*<sup>1</sup>

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Forty *Avena sativa* (L.) lines and 28 *A. sterilis* (L.) collections were evaluated in two nitrogen environments (i.e., low and high) for variation in nitrogen harvest index (NHI). Significant genetic variation for NHI occurred among entries within both species. NHI varied from 25 to 51%, with a mean of 42% for *A. sterilis*, and from 42 to 67%, with a mean of 59%, for *A. sativa*. Mean NHI was significantly lower in *A. sterilis* than in *A. sativa*. Some adapted entries with introgressed germplasm from *A. sterilis* had relatively high NHI's, however. Plant traits that were associated with NHI were harvest index (HI), groat yield (GTY), groat protein yield (GTPY), heading date (HD), and straw protein percentage (SP). High nitrogen fertility caused a significant decrease in NHI and HI, significant increases in groat protein percentage (GTP), straw yield (SY), SP, straw protein yield (SPY), total plant protein yield (TPPY), and vegetative growth rate (GR), and no change in GTY and GTPY for *A. sativa* entries. High nitrogen increased GTP, SY, SP, SPY, TPPY, and GR and decreased NHI and HI in *A. sterilis*.

INDEX DESCRIPTORS: Nitrogen harvest index, *Avena sativa*, *A. sterilis*, variation.

Increasing nitrogenous fertilizer costs and the emphasis on producing high protein cereal grain have generated interest in developing grain cultivars that are more efficient in nitrogen utilization.

Higher yielding cereals usually have a lower percentage of protein in the grain (Grant and McCalla, 1949); however, some genotypes do exhibit both higher yield and higher grain-protein percentage (Frey, 1977). To achieve this, such genotypes must either take up more nitrogen from the soil or translocate a greater proportion of the absorbed nitrogen into the grain. Most nitrogen in the grain of cereals is derived from the remobilization and translocation of vegetative nitrogen into the developing grain (Williams, 1955). Improving the efficiency of this process should increase grain-protein yields and, perhaps, break the inverse relationship between grain yield and grain-protein percentage in cereals grown with a limited supply of soil nitrogen (Dalling and Loyn, 1976). Indeed, some high-protein cultivars of cereals are more efficient than others in translocating nitrogen from vegetative organs to grain (Johnson et al., 1967; Perez et al., 1973; Peterson et al., 1975).

The partitioning efficiency of plant nitrogen between grain and straw has been called nitrogen harvest index (NHI) by Austin et al. (1977) and Desai and Bhatia (1978). NHI is the ratio of the weights of grain nitrogen to total plant nitrogen (excluding roots). NHI differences exist among cultivars of oats (*Avena sativa* L.), durum wheat (*Triticum durum* L.), and winter wheat (*T. aestivum*) (Wiggins and Frey, 1956; Desai and Bhatia, 1978; Austin et al., 1977).

Some studies have shown a negative relationship between grain-protein percentage and yield (Terman, 1979), while others have suggested that this relationship may be due to limited soil nitrogen (Hageman et al., 1976). Increasing the level of nitrogen fertilization causes greater percentages of grain-protein (Johnson et al., 1973) and straw-protein (Eagles et al., 1978) in cereals, but usually decreases the NHI (Wiggins and Frey, 1956).

Genes from some collections of *Avena sterilis*, a weedy oat species from the Middle East, have been used to elevate groat-protein percentage in cultivated oats (Frey, 1977). Further, considerable variation exists for straw-protein percentage among *A. sterilis* genotypes (Frey et al., 1975), but no data have been reported for NHI values of this species.

The objectives of this study were (a) to survey *Avena sativa* and *A. sterilis* genotypes for variation in NHI, (b) to determine the relation-

ship of NHI to other traits, and (c) to assess the effect of nitrogen fertilization on the expression of NHI and other traits.

## MATERIALS AND METHODS

Forty *A. sativa* lines and 28 *A. sterilis* collections were evaluated to assess the variation for NHI within these 2 species. *A. sterilis* collections represented wide ranges of groat- and straw-protein percentages and many geographic areas. The 13 *A. sativa* cultivars adapted to Iowa and that covered a range of protein percentages were 'Diana' (CI 7921), 'Grundy' (CI 8445), 'Cherokee' (CI 5444), 'Spear' (CI 9203), 'Dal' (CI 9159), 'Goodland' (CI 9202), 'Otee' (CI 9086), 'Lang' (CI 9257), 'Noble' (CI 9194), 'Stout' (CI 9195), 'Wright' (CI 9201), 'Clintford' (CI 7463), and CI 9170. Ten unadapted cultivars chosen from other countries were 'Craigs Afterlea' (CI 7317), A465, 'Black Rival' (CI 807), 'Cherinishvka' (CI 2059), 'Blanca Alemana' (CI 4506), 'Korean Native Oats' (CI 3456), 'Pusa Hybrid X27' (CI 3442), 'Golden Giant Liguleless' (CI 1606), CI 2109, and CI 2410. Eight high-protein lines with accessions B525 and B590 were derived from a bulk population made by compositing F<sub>2</sub> seed of 12 three-way oat matings. The remaining 9 *A. sativa* genotypes with high groat protein were selected from the Iowa program to introgress *A. sterilis* germplasm into cultivated oats.

On 18 April 1979, the 68 oat entries were sown in 2 experiments on a Coland loam (Cumulic Haplaquolls) soil on the Skunk River flood plain near Ames, Iowa. Soybeans were grown the previous year in the experimental area. The 2 experiments were treated identically except for level of nitrogen (N) fertilization. Each was sown in a randomized complete-block design with 4 replicates, and the experiments were grown contiguously. A plot consisted of 10 seeds sown in a hill, with hills spaced 30.5 cm apart in perpendicular directions. Two rows of border hills were planted around each experiment to provide competition for peripheral plots.

Soil samples were taken to a 6-inch (15 cm) depth from the experimental areas, placed in cold storage, and analyzed for organic matter percentage. The soil areas used for the LOW-N and HIGH-N experiments contained 3.1% and 2.3% organic matter, respectively. For the HIGH-N experiment, N, P<sub>2</sub>O<sub>5</sub>, and K<sub>2</sub>O were topdressed 1 week after planting at the rate of 112-75-75 kg/ha. To assure an adequate supply of N, an additional application of 112 kg/ha of N was made on 31 May (approximately 2 weeks before the earliest entries headed). Plants in each plot of this experiment were tied to stakes to prevent lodging. In the LOW-N experiment, P<sub>2</sub>O<sub>5</sub>, and K<sub>2</sub>O were each applied at the rate of 75 kg/ha.

The experiments were irrigated when necessary to insure that the

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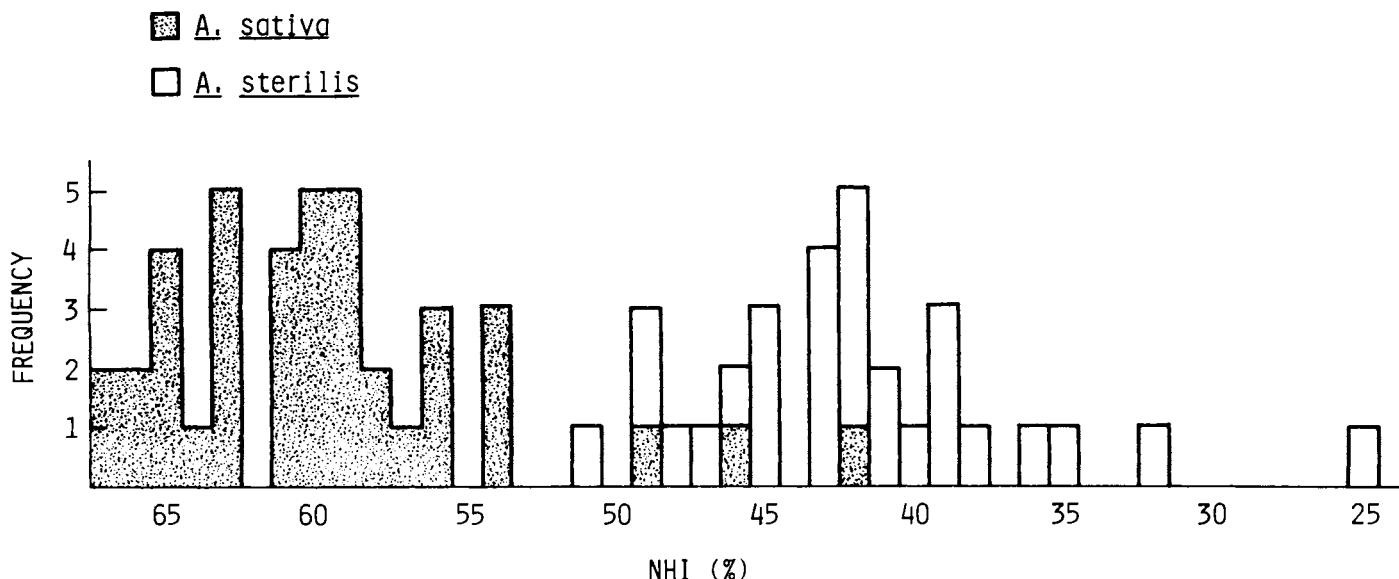


Figure 1. Frequency distributions (averaged across experiments) of NHI values for strains of *Avena sativa* and *A. sterilis*.

moisture level would be adequate for growth and uptake of nitrogen. Plants were sprayed with a fungicide at weekly intervals from anthesis to maturity to control foliar diseases, and heads of the *A. sterilis* entries were bagged shortly after anthesis with delnet PG218 nonwoven mesh bags (hi-density polyethylene mfg. by Hercules, Inc., Wilmington, DE 19899) to catch shattered seeds.

At maturity, plants in a plot were harvested at ground level, air-dried, and weighed to give bundle weight (BWT). Subsequently, the bundle of culms was threshed, and grain yield (GY) was recorded. Straw yield (SY<sub>2</sub>) was calculated as BWT-GY, and vegetative growth rate (GR) was computed as SY<sub>2</sub> divided by growth duration to heading. Heading date (HD) was the number of days after sowing when 50% of the panicles in a plot were fully emerged. All plot yields were recorded as g/plot and converted to q/ha.

Because *A. sterilis* seeds have a much higher hull percentage than do those from *A. sativa*, traits were calculated with hulls considered as a component of the straw. This made data from the 2 species comparable. From each plot, 10 seeds were randomly chosen, weighed, and dehulled, after which the dehulled groats (caryopses) were weighed, and a groat percentage (GP) was calculated. Groat yield (GTY) was computed as GY•GP, and hull yield (HY) was calculated as GY•(1-GP). Straw yield, including the hulls (SY), was calculated as SY<sub>2</sub>+HY, and harvest index (HI) was calculated as (GTY/BWT)•100.

Straw from each plot was ground to pass through a 15-mesh sieve, and the ground samples for an entry from replicates 1 and 2 were bulked to form one protein-replicate, and samples from replicates 3 and 4 were combined to form a second protein-replicate. The groats were combined similarly. Groat-N percentage was determined by using a micro-Kjeldahl procedure, as described by Cataldo et al. (1974), eliminating the predigestion step. Straw-N percentage was determined with the Neo-Tec Model 41 near-infrared analyzer. Groat protein percentage (GTP) and straw protein percentage (SP) were calculated by multiplying the respective N percentages by 6.25. Groat protein yield (GTPY) was calculated as GTY•GTP; straw protein yield was SY•SP; and total plant protein yield (TPPY) was com-

puted as GTPY + SPY. Nitrogen harvest index (NHI) was calculated as (GTPY/TPPY)•100.

Before the data were analyzed, means for all traits were computed for replicates one and two and for replicates three and four. This was done so that replicates for all traits would correspond to the protein replicates. Thus, an experiment was analyzed as though it had 2 replicates rather than 4. Analyses of variance were computed for each trait in each experiment, and since the error mean squares from the 2 experiments were homogeneous for each trait, combined analyses were conducted for each trait. Phenotypic correlations were computed for each pair of traits within each species by using mean values from the 2 N levels.

## RESULTS AND DISCUSSION

### Reactions within N Environments

NHI varied from 25 to 51% with a mean of 42% among the 28 *A. sterilis* entries, and from 42 to 67%, with a mean of 59% among the 40 *A. sativa* entries (Fig. 1, Table 1). The 2 species differed significantly for NHI, and there was significant variation for this trait in both species. The 10 unadapted *A. sativa* cultivars from other countries tended to have low NHI values, whereas experimental lines developed in Iowa and the adapted cultivars had high NHI's. The considerable genetic variation for NHI within both *A. sativa* and *A. sterilis* indicates that this trait could likely be manipulated up or down via selection.

There was no significant difference between the species means for SPY in either the HIGH-N or LOW-N experiments, but the GTP's and SP's were greater for *A. sterilis* in both experiments (Tables 1, 2). All other trait values were significantly greater for *A. sativa* in both experiments. Significant variation existed among entries within each species in the HIGH-N experiment for all 10 traits. Likewise in the LOW-N experiment, *A. sterilis* entries varied significantly for all traits, and *A. sativa* entries for all except SP and SPY.

HIGH-N caused a significant decrease in NHI, no change in GTY and GTPY, and significant increases in the other 7 traits for *A. sativa*

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Table 1. Mean of 10 traits for *A. sativa* and *A. sterilis* entries in the LOW-N and HIGH-N experiments.

Trait	Abbreviation	Unit of measure	<i>A. sativa</i>		<i>A. sterilis</i>	
			LOW-N	HIGH-N	LOW-N	HIGH-N
Nitrogen harvest index	NHI	%	63	55**	44	39
Groat yield	GTY	q/ha	32	30	13	14
Groat protein percentage	GTP	%	17.1	18.6*	20.7	21.9
Straw yield	SY	q/ha	67	73*	49	53
Straw protein percentage	SP	%	4.8	6.2**	7.0	8.7
Groat protein yield	GTPY	q/ha	5.4	5.6	2.7	2.9
Straw protein yield	SPY	q/ha	3.1	4.5**	3.3	4.4
Total plant protein yield	TPPY	q/ha	8.5	10.1*	5.9	7.3
Harvet index	HI	%	33	30*	21	20
Vegetative growth rate	GR	g/plot/da	0.83	0.97**	0.43	0.51

\*\*, \*, \*Indicate significant differences between the HIGH-N and LOW-N treatments at the 1%, 5%, and 10% levels, respectively.

Table 2. Levels of significance for 10 traits from analyses of variance for the HIGH-N and LOW-N environments, and from the combined analysis.

Source of Variation	Degrees of freedom	MEAN SQUARES									
	NHI	GTY	GTP	SY	SP	GTPY	SPY	TPPY	HI	GR	
HIGH-N Experiment											
<i>A. sativa</i> vs. <i>A. sterilis</i>	1	**	**	**	**	**	**	NS	**	**	**
Entries/ <i>A. sativa</i>	39	**	**	*	**	**	**	**	**	**	**
Entries/ <i>A. sterilis</i>	27	**	**	*	**	*	**	**	**	**	**
LOW-N Experiment											
<i>A. sativa</i> vs. <i>A. sterilis</i>	1	*	**	**	**	**	**	NS	**	**	**
Entries/ <i>A. sativa</i>	39	*	**	**	**	NS	**	NS	**	**	**
Entries/ <i>A. sterilis</i>	27	**	**	*	**	*	**	**	**	**	**
Combined Analysis											
Nitrogen level/ <i>A. sativa</i>	1	**	NS	NS	*	**	NS	**	*	NS	**
Nitrogen level/ <i>A. sterilis</i>	1	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS
Species x nitrogen level	1	*	*	NS	NS	NS	NS	NS	NS	**	*
Entries/ <i>A. sativa</i> x nitrogen level	39	NS	*	NS	NS	NS	*	NS	NS	*	NS
Entries/ <i>A. sterilis</i> x nitrogen level	27	*	**	NS	**	NS	**	**	**	NS	**

NS, \*, and \*\* Designate that mean squares were not significant and significant at the 5% and 1% levels, respectively.

(Table 1). None of the trait means was significantly changed for *A. sterilis* by the HIGH-N treatment, probably because significant replicate effects occurred for all traits. The replicate mean squares were used as error terms to test N effects, and because they were so large, no significant N level effects were found. However, there were trends for increases in GTP, SY, SP, SPY, TPPY, and GR, and decreases in NHI and HI due to high N application (Table 1).

A high level of N fertilization increased SY and SP relatively more than GTY and GTP in both species. In fact, the lower GTY's in the HIGH-N environment for *A. sativa* entries indicate that N fertilization may have increased vegetative growth at the expense of grain production, with the resultant reduction in HI and NHI.

Significant negative correlations existed between GTY and GTP for both species in the LOW-N and HIGH-N environments. This is contrary to the report by Hageman et al. (1976) that the negative correlation between grain-protein percentage and grain yield may have been due to limited soil N. However, it supports the findings of

Terman (1979) who found that the strong negative relationship between grain-protein percentage and grain yield for 6 wheat cultivars occurred at all soil nitrogen levels from very low to very high.

A significant entry by N level interaction existed for GTY for both species. It is noteworthy that *A. sativa* entries with high NHI's in the HIGH-N environment tended to have reduced GTY's in the LOW-N environment, whereas those with low NHI's in the HIGH-N environment tended to have higher GTY's in the LOW-N environment. The 10 entries with the highest NHI's in the HIGH-N environment had mean GTY's of 31.6 and 29.1 q/ha in the HIGH-N and LOW-N environments, respectively, a decrease of 2.5 q/ha. In contrast, the 10 with lowest NHI's in the HIGH-N environment had mean GTY's of 27.8 and 32.8 q/ha in the HIGH-N and LOW-N environments, respectively, an increase of 5.0 q/ha. This relationship is shown further by negative correlations between NHI in the HIGH-N environment and the GTY difference between N treatments (i.e.,

**Table 3. NHI values in the LOW-N and HIGH-N experiments and means across experiments for the 10 *A. sativa* and 10 *A. sterilis* entries highest in NHI.**

Entry <sup>a</sup>	EXPERIMENT		Mean
	LOW-N	HIGH-N	
<i>A. savtia</i>			
Cherokee (CI 5444) <sup>c</sup>	74(1) <sup>b</sup>	59(14)	67
Diana (CI 7921)	72(2)	61(7)	67
CI 9170	67(8)	65(1)	66
Otee (CI 9086)	67(8)	64(2)	66
B525-73 <sup>d</sup>	69(4)	61(7)	65
B525-76	68(5)	62(6)	65
B590-801	67(8)	63(4)	65
Spear (CI 9203)	65(15)	64(2)	65
Y20-3-8	68(5)	60(10)	64
B525-336	71(3)	55(23)	63
<i>A. sterilis</i>			
PI 412494	51(3)	50(1)	51
PI 411505	49(7)	49(2)	49
PI 411516	51(3)	47(4)	49
PI 298151	51(3)	44(7)	48
PI 412542	55(1)	38(19)	47
PI 412293	52(2)	40(12)	46
PI 320801	44(14)	46(5)	45
PI 411614	42(18)	48(3)	45
PI 412368	51(3)	38(19)	45
PI 324776	46(9)	39(14)	43

<sup>a</sup>Entries are arranged in order of decreasing overall NHI mean.

<sup>b</sup>Numbers in parentheses indicate rank for NHI of 40 entries for *A. sativa* and 28 entries for *A. sterilis*.

<sup>c</sup>CI refers to Cereal Index Number registered with the U.S. Department of Agriculture.

<sup>d</sup>B and Y are prefixes of oat strain accession numbers in the Iowa Agriculture and Home Economics Experiment Station.

GTY<sub>LOW-N</sub>-GTY<sub>HIGH-N</sub>). They were -0.30 for *A. sativa* and -0.28 for *A. sterilis*. This relationship indicates that entries with low NHI in the HIGH-N environment increased vegetative growth at the expense of grain production and, thus, gave higher GTY's with low applications of N. In contrast, entries with high NHI in the HIGH-N environment may require large amounts of N to sustain their GTY's. Probably, this relationship caused the entry by N level interaction for GTY in both species.

The fact that many *A. sativa* entries with high NHI's in the HIGH-N environment had reduced GTY's in the LOW-N environment suggests that some oat genotypes may be too efficient in translocating N from vegetative organs to grain. A possible explanation for this phenomena is that the cultivars with a high NHI may senesce prematurely causing an early and rapid translocation of N from the straw to the grain with the result that photosynthate is not produced for translocation to the grain.

Mikesell and Paulsen (1971) found that high-protein lines of wheat required continued assimilation of nitrogen by flag leaves after anthesis, and Ellen and Spiertz (1975) found that benzimidazole fungicides, which delay leaf senescence, increase the N content of wheat plants. Such results support the concept that lines selected for high NHI may be those with hastened senescence and resultant low GTY's when soil N is limited.

Significant entry by N level interactions were also found for GTPY and HI in *A. sativa*, and for NHI, SY, GTPY, SPY, TPHY, and GR in *A. sterilis*. The entry by N level interaction for NHI for *A. sativa* was not significant; nevertheless, some entries were not consistent for NHI across N levels. For example, B525-336 ranked third for NHI in the LOW-N and 23rd in the HIGH-N experiment (Table 3). Even though large changes in the ranking of cultivars were observed, the correlations between N environments for NHI were 0.67\*\* and 0.47\*\* for *A. sativa* and *A. sterilis*, respectively. Correlations between N levels for GTY, GTP, SY, and SP were 0.77\*\*, 0.54\*\*, 0.54\*\*, and 0.87\*\*, respectively, for *A. sativa*, and 0.74\*\*, 0.56\*\*, 0.61\*\*, and 0.73\*\*, respectively, for *A. sterilis*.

#### Associations among Traits

Because the expression of all traits was similar at the 2 N levels, mean values from the 2 environments were used to compute correlations between traits. High positive correlations were found between HI and NHI, between GTY and GTPY, and between SY and SPY within both species (Table 4), but no association existed between GTP and GTPY or between SP and SPY within *A. sativa*. There were significant, but low, negative correlations between GTP and GTPY and between SP and SPY for *A. sterilis*. Perhaps these were indirect manifestations of the strong negative correlations between GTP and GTY and between SP and SY. Takeda and Frey (1979) also found a strong association between grain protein yield (GPY) and grain yield, but a weak one between GPY and grain protein percentage in oats. These associations indicate that, generally, protein yields for both grain and straw were influenced more by dry-matter production than by protein concentrations.

Positive, but insignificant, correlations were found for NHI with GTY and GTP within *A. sativa*. However, the correlation of NHI with GTY approached significance and was significantly positive in the LOW-N experiment, suggesting that selecting for high NHI may

**Table 4. Correlations among traits with *A. sativa* and *A. sterilis* across two nitrogen levels.**

SPECIES	Trait	NHI	GTP	GTY	SP	SY
<i>A. sativa</i>	GTP	0.21	—	—	—	—
<i>A. sterilis</i>	GTP	-0.25	—	—	—	—
<i>A. sativa</i>	GTY	0.27	-0.48**	—	—	—
<i>A. sterilis</i>	GTY	0.64**	-0.59**	—	—	—
<i>A. sativa</i>	SP	-0.59**	0.05	-0.47*	—	—
<i>A. sterilis</i>	SP	-0.61**	0.32	-0.64**	—	—
<i>A. sativa</i>	SY	-0.23	-0.31*	0.76**	-0.40**	—
<i>A. sterilis</i>	SY	0.30	-0.39*	0.86**	-0.63**	—
<i>A. sativa</i>	GTPY	0.40*	-0.14	0.93**	-0.53**	0.73**
<i>A. sterilis</i>	GTPY	0.64**	-0.42*	0.97**	-0.65**	0.90**
<i>A. sativa</i>	SPY	-0.49**	-0.31	0.63**	-0.02	0.92**
<i>A. sterilis</i>	SPY	0.12	-0.34	0.77**	-0.41*	0.96**
<i>A. sativa</i>	TPPY	0.00	-0.24	0.89**	-0.34*	0.91**
<i>A. sterilis</i>	TPPY	0.40*	-0.40*	0.91**	-0.55**	0.97**
<i>A. sativa</i>	HI	0.76**	-0.11	0.20	-0.10	-0.45**
<i>A. sterilis</i>	HI	0.53**	-0.14	0.04	0.02	-0.27
<i>A. sativa</i>	GR	0.03	-0.38*	0.82**	-0.36*	0.78**
<i>A. sterilis</i>	GR	0.52**	-0.52**	0.94**	-0.65**	0.89**
<i>A. sativa</i>	HD	-0.44**	-0.12	0.34*	-0.28	0.79**
<i>A. sterilis</i>	HD	-0.53**	0.19	-0.11	0.02	0.26

\* and \*\* Designate that correlations are significant at the 5% and 1% levels, respectively.

break the inverse relationship between GTY and GTP within this species. For *A. sterilis*, a strong positive correlation was found between NHI and GTY, whereas a negative, but insignificant correlation was found between NHI and GTP. Other studies also showed no significant correlation between GTP and NHI (Desai and Bhatia, 1978; T. S. Cox, Department of Agronomy, Iowa State University, unpublished data).

TPPY and NHI were not correlated within *A. sativa*, which suggests that N uptake and N partitioning were controlled by separate physiological mechanisms. Desai and Bhatia (1978) found no correlation between TPPY and NHI in durum wheat either. A slight, but significant correlation (0.40\*) was found between TPPY and NHI for *A. sterilis*. GTPY and NHI were positively correlated for both species. SPY and NHI were negatively correlated for *A. sativa*, but not associated for *A. sterilis*. Strong negative correlations occurred between SP and NHI for both species, but SP and HI were not significantly correlated in either species. NHI and HD were significantly and negatively correlated in both species. Therefore, it seems that the major factors contributing to variation in NHI, directly or indirectly, within both *Avena* species were HI, GTY, GTPY, HD, and SP.

The strong positive correlations between NHI and GTPY showed that NHI would be useful for increasing the GTPY within both species. Of course, GTPY is the numerator of the formula used to compute NHI, so selection for GTPY would occur directly when one selected for NHI. However, a high GTPY would not necessarily mean efficient use of N taken up by the plant. If SPY was higher than necessary to meet the demands of grain, N would not be used efficiently, which would be especially critical in a situation in which available N was limited.

Negative correlations between SY and SP and between GTY and SP occurred for both species. SP and HD were not significantly correlated within either species, which contrasts to the high positive correlations found by Campbell and Frey (1974).

Mean NHI was lower in *A. sterilis* than in *A. sativa*, partly because of the lower GTY and HI characteristic of *A. sterilis*. These results suggest that *A. sterilis* germplasm would be of limited usefulness for increasing the NHI of *A. sativa*. However, some entries from the Iowa *A. sterilis* introgression program (e.g., Y20-3-8) have relatively high NHI's, which shows, as with other traits, that the usefulness of *A. sterilis* germplasm for improving cultivated oats cannot be predicted until genes from this species are substituted into an *A. sativa* genetic background.

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